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OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 22:19:34 ; Search time 504 Seconds
(Without alignments)
9579.929 Million cell updates/sec

Title: US-09-698-781-2
Perfect score: 2144
Sequence: 1 tgaatgaacaatacttcac.....gaaaaaaaaaaaaa 2144

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: N_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
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13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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15: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2144	100.0	2144	22	AAD06222	Human full-length
2	2126.6	99.2	2133	22	AAH98651	Human EST-derived
3	2126.6	99.2	2133	22	AAH98659	Human EST-derived
4	2113.2	98.6	2128	24	ABL67806	Oesophagus cancer
5	2100	97.9	2452	23	ABV22644	Human prostate exp
6	2100	97.9	2452	23	ABV24631	Human prostate exp
7	2100	97.9	2452	23	ABV25272	Human prostate exp
8	2100	97.9	2452	23	ABV25706	Human prostate exp
9	2100	97.9	2452	23	ABV28467	Human prostate exp

10	2100	97.9	2452	23	ABV28648	Human prostate exp
11	1130.6	52.7	1610	23	ABV24823	Human prostate exp
12	569.4	26.6	677	23	ABV38130	Human prostate exp
13	561.4	26.2	676	23	ABV08230	Human prostate exp
14	513.6	24.0	1386	23	AA570843	DNA encoding novel
15	513.6	24.0	1386	23	AA592411	DNA encoding novel
16	502.4	23.4	806	22	AA17940	Human breast cancer
17	469	21.9	619	23	ABV38778	Human prostate exp
18	467.6	21.8	668	22	AA124794	Human breast cancer
19	455	21.2	524	23	ABV08888	Human breast cancer
20	393.8	18.4	632	22	AA15950	Human breast cancer
21	391.4	18.3	534	23	ABV43214	Human prostate exp
22	367.8	17.2	460	23	ABV43523	Human prostate exp
23	302.6	14.1	410	23	ABV37438	Human prostate exp
24	302.4	14.1	372	23	ABV13234	Human prostate exp
25	300	14.0	395	23	ABV34353	Human prostate exp
26	254.6	11.9	683	23	AA570842	DNA encoding novel
27	254.6	11.9	683	23	AA592408	DNA encoding novel
28	254.4	11.9	256	22	AAD06221	Human 36P1G3 cDNA.
29	248.2	11.6	371	22	AA110867	Human breast cancer
30	222	10.4	817	23	ABV06525	Human breast cancer
31	212.4	9.9	263	20	AA40711	Human secreted pro
32	205.6	9.6	371	23	ABV07505	Human prostate exp
33	200.6	9.4	343	23	ABV08331	Human prostate exp
34	200.6	9.4	395	23	ABV38239	Human prostate exp
35	198.4	9.3	633	23	ABV37142	Human prostate exp
36	198	9.2	540	23	ABV08906	Human prostate exp
37	197.4	9.2	400	23	ABV07202	Human prostate exp
38	196	9.1	430	23	ABV08865	Human prostate exp
39	196	9.1	451	23	ABV38756	Human prostate exp
40	174.4	8.1	530	23	ABV38795	Human prostate exp
41	173.8	8.1	282	23	ABV3790	Human prostate exp
42	170.4	7.9	2452	23	ABV22644	Human prostate exp
43	170.4	7.9	2452	23	ABV24631	Human prostate exp
44	170.4	7.9	2452	23	ABV25272	Human prostate exp
45	170.4	7.9	2452	23	ABV25706	Human prostate exp

ALIGNMENTS

RESULT 1	
AAD06222	
ID	AAD06222 standard; cDNA: 2144 BP.
AC	AAD06222;
XX	31-JUL-2001 (first entry)
DT	
XX	Human full-length 36P1G3/SGP28 cDNA.
DE	
KW	Human: 36P1G3 clone; specific granule protein 28; SGP28; therapy;
KW	prostate; colon; cancer; prognosis; vaccine; anticancer; ss.
XX	
OS	Homo sapiens.
XX	
FX	
FT	Key
FT	CDS
FT	
FT	sig_peptide
FT	3..98
FT	/tag- a
FT	/product- "Human full-length 36P1G3/SGP28 protein"
FT	mat_peptide
FT	99..776
FT	/tag- b
FT	/tag- c
FT	/product- "Human mature full-length 36P1G3/SGP28 protein"
FT	
PN	WO200131343-A2.
PD	
XX	03-MAY-2001.
XX	
PF	27-OCT-2000; 2000WO-US29607.
XX	
PR	28-OCT-1999; 99US-0162610.

XX (UROC-) UROGENESYS INC.
 PA Hubert RS, Raitano AB, Afar DEH, Mitchell SC, Paris M;
 PI Jakobovits A;
 PI WPI: 2001-308685/32.
 DR P-PSDB: AA02211.
 DR
 XX Detecting cancers, particularly of prostate and colon, from
 PT overexpression of SGP28 protein, also methods for treating these
 PT cancers e.g. by vaccination with the protein
 PS Claim 16: Page 62-63; 102pp; English.
 XX
 CC The present invention relates to methods and compositions for the
 CC diagnosis and therapy of prostate cancer which utilize human SGP28
 CC (specific granule protein 28) gene and proteins. The method involves
 CC detecting cancers, particularly of prostate and colon, from
 CC overexpression of SGP28 protein. The expression of SGP28, which is an
 CC extracellular protein is restricted to the prostate and ovary, and is
 CC markedly up-regulated in prostate tumours. SGP28 sequence is used for
 CC diagnosis (including in vivo imaging), staging, monitoring and prognosis
 CC of prostate and colon cancer, and for assisting selection of therapy.
 CC Also SGP28 expressing cancers can be treated by administering a
 CC composition or vaccine that contains a vector expressing an antibody
 CC specific for SGP28 protein, nucleic acid encoding SGP28 protein or its
 CC fragments, polypeptides encoded by SGP28 gene and SGP28-specific antibody
 CC is also used as source of therapeutic antisense or ribozyme agents, as
 CC primers/probes for diagnosis or prognosis, to identify compounds that
 CC inhibit calcium entry into prostatic cells, for recombinant production
 CC of SGP28 peptides and for isolating related sequences. SGP28 protein and
 CC its fragments are used to raise specific antibodies (Ab) and to identify
 CC specific binding agents (potentially useful as therapeutic and
 CC diagnostic agents) and also potential anticancer agents. The present
 CC sequence is human full-length 36163/SGP28 cDNA.
 XX
 SO Sequence 2144 BP; 735 A; 403 C; 382 G; 624 T; 0 other;
 Query Match 100.0%; Score 2144; DB 22; Length 2144;
 Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 2144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 TAGGGCCAAAGACTCCCAAGCCAGTGGTGGACATTATACAGAGTGGTGGTACTCTT 480
 QY 481 CATACCTCGTGGATGTAAGAAATGCTACTGTCCCAATCAAAAGTCTAAATACTACT 540
 DB 481 CATACCTCGTGGATGTAAGAAATGCTACTGTCCCAATCAAAAGTCTAAATACTACT 540
 QY 541 ATGTTGCCAATATGTCTGCTGGTAAATGGGCTAATAGATATATGCTTATGAC 600
 DB 541 ATGTTGCCAATATGTCTGCTGGTAAATGGGCTAATAGATATATGCTTATGAC 600
 QY 601 AAGAGCACCCTTGCCAGTGGCCCAATATCTGACAGATGACTATGACCAATGGTT 660
 DB 601 AAGAGCACCCTTGCCAGTGGCCCAATATCTGACAGATGACTATGACCAATGGTT 660
 QY 661 GCAAGTGAAGATCTATATAGTAACTGTAAGTGAAGCTGACATTAACCTGTAAC 720
 DB 661 GCAAGTGAAGATCTATATAGTAACTGTAAGTGAAGCTGACATTAACCTGTAAC 720
 QY 721 ATCAGTTGGTCAGGAGAGTTCGAAGCATCCTGCAATGTTCAAGCATTATTTAA 780
 DB 721 ATCAGTTGGTCAGGAGAGTTCGAAGCATCCTGCAATGTTCAAGCATTATTTAA 780
 QY 781 TACCATTTACACCCGATAGGCTATGTAGAGAGAGTCAATATCTACTTATGATTGG 840
 DB 781 TACCATTTACACCCGATAGGCTATGTAGAGAGAGTCAATATCTACTTATGATTGG 840
 QY 841 GCATCTCTTATGATTTATACATATATCTAGCTGAGAAATTTGAGCATTTGATACATTT 900
 DB 841 GCATCTCTTATGATTTATACATATATCTAGCTGAGAAATTTGAGCATTTGATACATTT 900
 QY 901 TGATTTCAAAATGTTTTCTCTGATGCTGCTTTTATTTACAAAATATTTTTCATACA 960
 DB 901 TGATTTCAAAATGTTTTCTCTGATGCTGCTTTTATTTTCAAAAATATTTTTCATACA 960
 QY 961 AATGTTTAAAGAAACAAATCTATACAAACAACTTGGATTTTATATTAACCTTTG 1020
 DB 961 AATGTTTAAAGAAACAAATCTATACAAACAACTTGGATTTTATATTAACCTTTG 1020
 QY 1021 TGATTTAAATTTACTGATTTAATAGGGTGAATTTTGAAGTGTATTCCTATGTA 1080
 DB 1021 TGATTTAAATTTACTGATTTAATAGGGTGAATTTTGAAGTGTATTCCTATGTA 1080
 QY 1081 CTAAGTTCATTAACCTTGATTAAGAAATGTAATATGTTCTTAGAACAAATGTACA 1140
 DB 1081 CTAAGTTCATTAACCTTGATTAAGAAATGTAATATGTTCTTAGAACAAATGTACA 1140
 QY 1141 AAAAAGCAATATATTTTACATGAACCTTGCTGATGCTGCTTCTAGCTCACT 1200
 DB 1141 AAAAAGCAATATATTTTACATGAACCTTGCTGATGCTGCTTCTAGCTCACT 1200
 QY 1201 CTAAGGCTAAGCATCTTCAAGAGCTTTTCCCATATGCTGCTTAATCTTTTACATCAT 1260
 DB 1201 CTAAGGCTAAGCATCTTCAAGAGCTTTTCCCATATGCTGCTTAAATCTTTTACATCAT 1260
 QY 1261 TCACCTTCTTCCCAATCATCTGCTGCAATCTCCACAAATGATGAGGTGCTCTCC 1320
 DB 1261 TCACCTTCTTCCCAATCATCTGCTGCAATCTCCACAAATGATGAGGTGCTCTCC 1320
 QY 1321 TAAACAATCTGACTTTTATTTTGGCCAAATCAATACATCTTTGAATTTTATCTG 1380
 DB 1321 TAAACAATCTGACTTTTATTTTGGCCAAATCAATACATCTTTGAATTTTATCTG 1380
 QY 1381 CATAAATTTTACATAGATATGATCAAACTTATTTTAACTCTCTCTCTGAC 1440
 DB 1381 CATAAATTTTACATAGATATGATCAAACTTATTTTAACTCTCTCTCTGAC 1440
 QY 1441 AAAAATCTCTTAAAAAAGATACAGATATATAGTAAATACCTTCAAGAGGT 1500
 DB 1441 AAAAATCTCTTAAAAAAGATACAGATATATAGTAAATACCTTCAAGAGGT 1500
 QY 1501 AGAATCTAGTCTCTCTCTGATGCTTCACTAAATCAAGTCACTCTTCAAGAGT 1560
 DB 1501 AGAATCTAGTCTCTCTCTGATGCTTCACTAAATCAAGTCACTCTTCAAGAGT 1560

QY 722 TCAGTTGGTCAGGAGACAGTTGCAAGCATCTCGCAATTTGTCAACAGCATTTATTAAT 781
 DB 721 TAGGTGGTCAGGAGAGAGTTGCAAGCATCTCGCAATTTGTCAACAGCATTTATTAAT 780
 QY 782 ACGCATTTACACACGAGTGGGCTATGTAGAGAGAGTGAATTAATCTAGTATGATTTG 841
 DB 781 ACGCATTTACACACGAGTGGGCTATGTAGAGAGAGTGAATTAATCTAGTATGATTTG 840
 QY 842 CATCTACTAGATTAACTATAGTACTGAGAAATTTGAGCATGTTTGATACACATTT 901
 DB 841 CATCTACTAGATTAACTATAGTACTGAGAAATTTGAGCATGTTTGATACACATTT 900
 QY 902 GATTTCAATGTTTTCTCTGATCTGTTTTATTTTACAAAATATTTTCATACA 961
 DB 901 GATTTCAATGTTTTCTCTGATCTGTTTTATTTTACAAAATATTTTCATACA 960
 QY 962 ATGTTTAAAAAGAACAAATCTATACACACACTTGGATTTTATATATAAGTTGT 1021
 DB 961 ATGTTTAAAAAGAACAAATCTATACACACACTTGGATTTTATATATAAGTTGT 1020
 QY 1022 GATTTAAATTTACTGAAATTTAATAGGGTAAATTTTGAAGTTGTATTTTCATATGAC 1081
 DB 1021 GATTTAAATTTACTGAAATTTAATAGGGTAAATTTTGAAGTTGTATTTTCATATGAC 1080
 QY 1082 TAAGTTCACTAAACCCCTGGATTTGAAAGTAAATTTATCTCTAGAACAAATGTACA 1141
 DB 1081 TAAGTTCACTAAACCCCTGGATTTGAAAGTAAATTTATCTCTAGAACAAATGTACA 1140
 QY 1142 AAAGAACATATATATTTTACATGACATGAAACCTTGGCTGATGCTCTTCTAGTCCACAGC 1201
 DB 1141 AAAGAACATATATATTTTACATGACATGAAACCTTGGCTGATGCTCTTCTAGTCCACAGC 1200
 QY 1202 TAAGGCTAAGCATCTTCAAGACGTTTCCATATGCTGCTTAAATCTTTTCACTCANT 1261
 DB 1201 TAAGGCTAAGCATCTTCAAGACGTTTCCATATGCTGCTTAAATCTTTTCACTCANT 1260
 QY 1262 CACCTTCTCCCAATCATCTGGTGGGATCTCTCAATTTGAGTGAAGCTTCTCTCT 1321
 DB 1261 CACCTTCTCCCAATCATCTGGTGGGATCTCTCAATTTGAGTGAAGCTTCTCTCT 1320
 QY 1322 AAAACAATCTGACTTTTATTTTGGCAAAATCAATACATCTTGAATTTTATATGTC 1381
 DB 1321 AAAACAATCTGACTTTTATTTTGGCAAAATCAATACATCTTGAATTTTATATGTC 1380
 QY 1382 ATAAATTTTACATGATATGATCAAACTTCATTTTAAACCTCTCTCTTTGACA 1441
 DB 1381 ATAAATTTTACATGATATGATCAAACTTCATTTTAAACCTCTCTCTTTGACA 1440
 QY 1442 AAATCTCTTAAAAAAGAAATCAAGATATATATAGTAAATACCCCTCACTCAAGAGATA 1501
 DB 1441 AAATCTCTTAAAAAAGAAATCAAGATATATATAGTAAATACCCCTCACTCAAGAGATA 1500
 QY 1502 GAATCACTCTCTCTCTCTGTGAGTCTTCACTAAATCAGTACTCACTTCCAAAGAGTG 1561
 DB 1501 GAATCACTCTCTCTCTCTGTGAGTCTTCACTAAATCAGTACTCACTTCCAAAGAGTG 1560
 QY 1562 GAGTATGGAAGGAAACATAGTAACTTTACAGGGGAGAAAAATGACAAATGACGCTCTTC 1621
 DB 1561 GAGTATGGAAGGAAACATAGTAACTTTACAGGGGAGAAAAATGACAAATGACGCTCTTC 1620
 QY 1622 ACCAAGTATCAAAATTAAGTCACAGTGAATTAAGTCAATTCAGATTTTCTCTAGATATC 1681
 DB 1621 ACCAAGTATCAAAATTAAGTCACAGTGAATTAAGTCAATTCAGATTTTCTCTAGATATC 1680
 QY 1682 TTTCTAAAAATTCATATCCCAATCTAATTAAGTCAATTCAGATTTTCTCTAGATATC 1741
 DB 1681 TTTCTAAAAATTCATATCCCAATCTAATTAAGTCAATTCAGATTTTCTCTAGATATC 1740
 QY 1742 GAAGGACATTTACAAATATCCCGGGGATTTTAAAGTATCTCTCAAAACTGTAAAAA 1801
 DB 1741 GAAGGACATTTACAAATATCCCGGGGATTTTAAAGTATCTCTCAAAACTGTAAAAA 1800

QY 1802 TCATGGAAAAATAGGGAATCTCTGAGAAACATCAGACACCATGAGACTAAGAGACAT 1861
 DB 1801 TCATGGAAAAATAGGGAATCTCTGAGAAACATCAGACACCATGAGACTAAGAGACAT 1860
 QY 1862 GTGAGCCAAATGCAATGTCTCTTGGATCAGATCTCTGGAACAGAAAAAGATCAATATG 1921
 DB 1861 GTGAGCCAAATGCAATGTCTCTTGGATCAGATCTCTGGAACAGAAAAAGATCAATATG 1920
 QY 1922 AAAAACTGATGATGCTCTGATAGATCTGAGATATTTTAAACAGTATGATTTCTT 1981
 DB 1921 AAAAACTGATGATGCTCTGATAGATCTGAGATATTTTAAACAGTATGATTTCTT 1980
 QY 1982 AATCTTGACAAATATAGCAGGTAATGTAAATGATTAACGTTAGAGAAACTGAACTGGG 2041
 DB 1981 AATCTTGACAAATATAGCAGGTAATGTAAATGATTAACGTTAGAGAAACTGAACTGGG 2040
 QY 2042 TGAGGGCTATCTAGGAATCTCTGATCTATCTTACCAATTTTCGGTAAAGTAAAG 2101
 DB 2041 TGAGGGCTATCTAGGAATCTCTGATCTATCTTACCAATTTTCGGTAAAGTAAAG 2100
 QY 2102 CAATGCAAAATTAAGAGTATCTTGAAGAAAAA 2134
 DB 2101 CAATGCAAAATTAAGAGTATCTTGAAGAAAAA 2133

RESULT 3
 AAH98659
 ID AAH98659 standard; cDNA: 2133 BP.
 XX
 XX AAH98659;
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST-derived coding sequence SEQ ID NO: 516.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition; ss.
 OS Homo sapiens.
 XX
 XX WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX
 DR WPI; 2001-476164/51.
 DR P-PSDB; AAM24000.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 XX
 PS Claim 1; Page 537-538; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA

Db 2041 TGAGGCTATCTAGCAATCTCTGACTTCTTACCAATTTTGGTAGTCTAAGAAG 2100
 OY 2102 CAATGCAAAATATAAAGTATCTTGAAAAA 2134
 |||||||
 Db 2101 CAATGCAAAATATAAAGTCTCAAAAAA 2133
 |||||||
 RESULT 4
 ABL67806
 ID ABL67806 standard; DNA: 2128 BP.
 XX
 AC ABL67806;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:6143.
 XX
 KM Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KM stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
 KM cytosolic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KM gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX

PA (AVAL-) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI: 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1: SEQ ID 6143; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61864
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytosolic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX
 SQ Sequence 2128 BP; 734 A; 397 C; 380 G; 617 T; 0 other;
 Query Match 98.6%; Score 2113.2; DB 24; Length 2128;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2115; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 27 CTGGAACCACTGCAATGACATTTATCCAGTGTGTTGCTGCTGGCTGCTT 86
 |||||||
 Db 1 CTGGAACCACTGCAATGACATTTATCCAGTGTGTTGCTGCTGGCTGCTT 60
 OY 87 CCATCTTTCCAGCAAAAGAGATAGATCCGCTTTTACTGCTTTTAAACCCCAA 146
 |||||||
 Db 61 CCATCTTTCCAGCAAAAGAGATAGATCCGCTTTTACTGCTTTTAAACCCCAA 120
 OY 147 ACACAAGTCAAAAGGAGATTTGTAATGAACCAATGAAGTGAAGAGAGATATCTCC 206
 |||||||
 Db 121 ACACAAGTCAAAAGGAGATTTGTAATGAACCAATGAAGTGAAGAGAGATATCTCC 180
 OY 207 CCTGCCAACAATGCTGTAAGATGGAATGAACCAAGGCTGCAACAATGCCCAAAG 266
 |||||||
 Db 181 CCTGCCAACAATGCTGTAAGATGGAATGAACCAAGGCTGCAACAATGCCCAAAG 240
 OY 267 TGGGCAAAACGATGCAATTAACAGACAGTAACCAAGGATCGAATACAGTATAAA 326
 |||||||
 Db 241 TGGGCAAAACGATGCAATTAACAGACAGTAACCAAGGATCGAATACAGTATAAA 300
 OY 327 TGTGGTGAAGATCTCTACATGTCAGAGTCCCACTGATGTCACAGCATCCAAAGC 386
 |||||||
 Db 301 TGTGGTGAAGATCTCTACATGTCAGAGTCCCACTGATGTCACAGCATCCAAAGC 360
 OY 387 TGTGGTGAAGATGATGATTTGACTTGTGTGAGGCAAAAGTCCCAAGCAGTG 446
 |||||||
 Db 361 TGTGGTGAAGATGATGATTTGACTTGTGTGAGGCAAAAGTCCCAAGCAGTG 420
 OY 447 GTTGACATTTATACACAGTGTGTTGAGTCTTATACCTCGTTGATGTGGAATGCC 506
 |||||||
 Db 421 GTTGACATTTATACACAGTGTGTTGAGTCTTATACCTCGTTGATGTGGAATGCC 480
 OY 507 TACTGTCCCAATCAAAAAGTCTTAAATACTATGTTTCCCAATATGCTGCTGCTG 566
 |||||||
 Db 481 TACTGTCCCAATCAAAAAGTCTTAAATACTATGTTTCCCAATATGCTGCTGCTG 540

QY 567 AATTGGCTAATAGACTATATGTCCCTATGAAACAAGGAGCACCCTGTGCCAGTTGCCA 626
 DB 541 AATTGGCTAATAGACTATATGTCCCTATGAAACAAGGAGCACCCTGTGCCAGTTGCCA 600
 QY 627 GATACTAGTGCAGTAGGACTATGACCAATGTTGCAAGTACGAGATCTCTATAGTAAC 686
 DB 601 GATACTAGTGCAGTAGGACTATGACCAATGTTGCAAGTACGAGATCTCTATAGTAAC 660
 QY 687 TGTAAAGTTGAAAGCTCACAATTAACCTGTAACATCACTGTTGGTGAAGGACAGTTGCAAG 746
 DB 661 TGTAAAGTTGAAAGCTCACAATTAACCTGTAACATCACTGTTGGTGAAGGACAGTTGCAAG 720
 QY 747 GCATCCCTGCATTTGTTCAACAAGCATTTATTAATAGCATTAACACCGAGTAGGGCTA 806
 DB 721 GCCTCTGCATTTGTTCAACAAGCATTTATTAATAGCATTAACACCGAGTAGGGCTA 780
 QY 807 TGTAGAGAGAGTGCAGATTATCTACTAGATTGGCATCTACTTATGATTATTAACATATCT 866
 DB 781 TGTAGAGAGAGTGCAGATTATCTACTAGATTGGCATCTACTTATGATTATTAACATATCT 840
 QY 867 AGCTGAGAAATTTGAGCATGTTGATACACATTTGATTGATTCAAATGTTTTCTCTGAT 926
 DB 841 AGCTGAGAAATTTGAGCATGTTGATACACATTTGATTGATTCAAATGTTTTCTCTGAT 900
 QY 927 CTGCTTTTATTTTACAAAATATTTTTCATACAAATGTTTAAAGAAACAAATCTAT 986
 DB 901 CTGCTTTTATTTTACAAAATATTTTTCATACAAATGTTTAAAGAAACAAATCTAT 960
 QY 987 AACAACTTTGATTTTATATATTAATTAACCTTGTGATTAAATTTAGCAATTAATTA 1046
 DB 961 AACAACTTTGATTTTATATATTAATTAACCTTGTGATTAAATTTAGCAATTAATTA 1020
 QY 1047 GGGTGAATAATTTGAAAGTTGATTTCTATTCATATGACTAAGTCACTAAACCTGATTTGA 1106
 DB 1021 GGGTGAATAATTTGAAAGTTGATTTCTATTCATATGACTAAGTCACTAAACCTGATTTGA 1080
 QY 1107 AAGTGAATAATTTGCTCTAGACAAATGTTACAAAGAAACAAATATTAATTTTCAATGA 1166
 DB 1081 AAGTGAATAATTTGCTCTAGACAAATGTTACAAAGAAACAAATATTAATTTTCAATGA 1140
 QY 1167 ACCCTTGGCTAGTGTGCTTCTAGCTCCACTAAGGCTAAGCATCTTCAAGAGCT 1226
 DB 1141 ACCCTTGGCTAGTGTGCTTCTAGCTCCACTAAGGCTAAGCATCTTCAAGAGCT 1200
 QY 1227 TTTCCCATATGCTGTCTTAATTTCTTTTCACTCATTCACCCCTCTTCCCATCATCTGGCT 1286
 DB 1201 TTTCCCATATGCTGTCTTAATTTCTTTTCACTCATTCACCCCTCTTCCCATCATCTGGCT 1260
 QY 1287 GGCATCCCTCACAATGAGTGAAGTGTCCCTTAAACAAATCCTGACTTTTATTTTTC 1346
 DB 1261 GGCATCCCTCACAATGAGTGAAGTGTCCCTTAAACAAATCCTGACTTTTATTTTTC 1320
 QY 1347 CAAAATCAATCAATCTTTGAATTTTATCTGCATTAATTTTACAGTAGAATATGATC 1406
 DB 1321 CAAAATCAATCAATCTTTGAATTTTATCTGCATTAATTTTACAGTAGAATATGATC 1380
 QY 1407 AAACCTTATTTTAAACCTCTCTCTCTTTTACAAAATCTTCTTAAAGAAATATCAAG 1466
 DB 1381 AAACCTTATTTTAAACCTCTCTCTCTTTTACAAAATCTTCTTAAAGAAATATCAAG 1440
 QY 1467 ATATATATGTTAAATACCTCCACTCAAGAGAGTAGAACTGCTCTCCCTGTGAGAT 1526
 DB 1441 ATATATATGTTAAATACCTCCACTCAAGAGAGTAGAACTGCTCTCCCTGTGAGAT 1500
 QY 1527 CTTCACATAAATCAGTGACTACTTCAAAAGATGAGATATGAAAGGAAACATATAGTA 1586
 DB 1501 CTTCACATAAATCAGTGACTACTTCAAAAGATGAGATATGAAAGGAAACATATAGTA 1560
 QY 1587 CTTTACAGGGGAGAAATGACAAATGAGCTTTTACCAAGTATCAAAATTAAGTCAAC 1646
 DB 1561 CTTTACAGGGGAGAAATGACAAATGAGCTTTTACCAAGTATCAAAATTAAGTCAAC 1620
 QY 1647 CAGTATATAGTATCAGATTTGTCTATAGATATATCTTTTAAAAATATCATATCCCAATC 1706

DB 1621 CAGTATATAGTATTCACATATTTGTTCTAGATATATCTTTCTAAAAATCATATATCCCAATC 1680
 QY 1707 TAATATAGCTTAAACATATCCAGCAAACTCAAGTTGAAGAGACTTCTACAAATATCCCT 1766
 DB 1681 TAATATAGCTTAAACATATCCAGCAAACTCAAGTTGAAGAGACTTCTACAAATATCCCT 1740
 QY 1767 GGGCTATTTTAGATATTCCTCAAAACCTGTAATTAATTCATGGAATATGAGGAATCTCTGAG 1826
 DB 1741 GGGCTATTTTAGATATTCCTCAAAACCTGTAATTAATTCATGGAATATGAGGAATCTCTGAG 1800
 QY 1827 AAACATCAACAGACCATGAGACTAAGAGACATGTGAGCCAAATGCAATGCTTCTT 1886
 DB 1801 AAACATCAACAGACCATGAGACTAAGAGACATGTGAGCCAAATGCAATGCTTCTT 1860
 QY 1887 GGATCAGATCCTGGAACAGAAAGAAATCAGTAATGAAAAAACTGATGAATCTGATAGA 1946
 DB 1861 GGATCAGATCCTGGAACAGAAAGAAATCAGTAATGAAAAAACTGATGAATCTGATAGA 1920
 QY 1947 ATCTGAGTATTTTAAAGAGTGTGATTTCTTAACTTAACTTGAACAAATATACAGAGTTA 2006
 DB 1921 ATCTGAGTATTTTAAAGAGTGTGATTTCTTAACTTGAACAAATATACAGAGTTA 1980
 QY 2007 TGTAGATGATTAACGTTAGAGAACTGAAACTGGGTGAGGGCTATCTAGAAATCTCTGT 2066
 DB 1981 TGTAGATGATTAACGTTAGAGAACTGAAACTGGGTGAGGGCTATCTAGAAATCTCTGT 2040
 QY 2067 ACTATCTTACCAAAATTTTGGTAACTCTAAGAAAGCAATGCAAAATTAAGATATCTTGA 2126
 DB 2041 ACTATCTTACCAAAATTTTGGTAACTCTAAGAAAGCAATGCAAAATTAAGATATCTTGA 2100
 QY 2127 AAAAAAAAAAAAAAAAAA 2144
 DB 2101 AAAAAAAAAAAAAAAAAA 2118

RESULT 5
 ABV22644
 ID ABV22644 standard; cDNA: 2452 BP.
 AC ABV22644;
 DT 13-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 22635.
 DE Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 KM Homo sapiens.
 OS
 XX WO200160860-A2.
 PN
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 XX
 PR 16-MAR-2000; 2000US-189862P.
 XX
 PR 25-MAY-2000; 2000US-207454P.
 XX
 PR 09-JUN-2000; 2000US-211314P.
 XX
 PR 18-JUL-2000; 2000US-219007P.
 XX
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer

QY 902 GATTCAATGTTTTCTCTGATCGCTTTTATTTTACAAAATATTTTCATACAA 961
 |||
 DB 1096 GATTCAAAATGTTTTCTCTGATCGCTTTTATTTTACAAAATATTTTCATACAA 1155
 |||
 QY 962 ATGGTAAAAAGAAACAAATCTATACAAACACTTTGGATTTTATATATAACTTTGT 1021
 |||
 DB 1156 ATGGTAAAAAGAAACAAATCTATACAAACACTTTGGATTTTATATATAACTTTGT 1215
 |||
 QY 1022 GATTAAATTTAGTGAATTAATTTAGGTAATAATTTGAAAGTGATATCTCATATGAC 1081
 |||
 DB 1216 GATTAAATTTAGTGAATTAATTTAGGTAATAATTTGAAAGTGATATCTCATATGAC 1275
 |||
 QY 1082 TAAGTCACTAAACCCCTGGATGAAAGTAAATATTTGTCAGAAACAAATGTACAA 1141
 |||
 DB 1276 TAAGTCACTAAACCCCTGGATGAAAGTAAATATTTGTCAGAAACAAATGTACAA 1335
 |||
 QY 1142 AAAGAACATATATATTTTTCATGATGAACCCCTGGCTAGTGGCTTCTAGCTCACATC 1201
 |||
 DB 1336 AAAGAACATATATATTTTTCATGATGAACCCCTGGCTAGTGGCTTCTAGCTCACATC 1395
 |||
 QY 1202 TAAGGCTAAGCATCTTCAAGAGCTTTCCCATATGCTGCTTATTTCTTTCACTCAT 1261
 |||
 DB 1396 TAAGGCTAAGCATCTTCAAGAGCTTTCCCATATGCTGCTTATTTCTTTCACTCAT 1455
 |||
 QY 1262 CACCTTCTTCCCAATCATCTGGCTGGCATCTCACAAATGAGTGAAGCTGTTCCCTCT 1321
 |||
 DB 1456 CACCTTCTTCCCAATCATCTGGCTGGCATCTCACAAATGAGTGAAGCTGTTCCCTCT 1515
 |||
 QY 1322 AAAACAATCTGACTTTTATTTTGGCAAAATCAATACATCTTTGATTTTATCTGC 1381
 |||
 DB 1516 AAAACAATCTGACTTTTATTTTGGCAAAATCAATACATCTTTGATTTTATCTGC 1575
 |||
 QY 1382 ATAAATTTTCAATAGATATGATCAAACTTATTTTAACTCTCTCTCTTTGACA 1441
 |||
 DB 1576 ATAAATTTTCAATAGATATGATCAAACTTATTTTAACTCTCTCTCTTTGACA 1635
 |||
 QY 1442 AAATCTCTTAAAAAAGAAATACAAAGATATATATGTAATACCTCCTCAGCAGAGGTA 1501
 |||
 DB 1636 AAATCTCTTAAAAAAGAAATACAAAGATATATATGTAATACCTCCTCAGCAGAGGTA 1695
 |||
 QY 1502 GAACTCAGTCTCTCCCTGTGAGTCTTCACTAAATTCAGTCACTCTCCAAAGAGTG 1561
 |||
 DB 1696 GAACTCAGTCTCTCCCTGTGAGTCTTCACTAAATTCAGTCACTCTCCAAAGAGTG 1755
 |||
 QY 1562 GAGTATGGAAGGAAACATAGTACTTTCACGGGAGAAAAATGACAAATGAGCTCTTC 1621
 |||
 DB 1756 GAGTATGGAAGGAAACATAGTACTTTCACGGGAGAAAAATGACAAATGAGCTCTTC 1815
 |||
 QY 1622 ACCAAGTGAATTAATGAGTACAGGATATGATTCATTCAGATTTGTTCTGATATATC 1681
 |||
 DB 1816 ACCAAGTGAATTAATGAGTACAGGATATGATTCATTCAGATTTGTTCTGATATATC 1875
 |||
 QY 1682 TTTCTAAAAATTCATATCCCAATCTAATTTATGAGCTAAACATCCAGCAAACTCAAGTT 1741
 |||
 DB 1876 TTTCTAAAAATTCATATCCCAATCTAATTTATGAGCTAAACATCCAGCAAACTCAAGTT 1935
 |||
 QY 1742 GAAGGACATTTCTACAAATATCCCTGGGATTTTATGAGATTTCTCTCAAAACTGTAAAAA 1801
 |||
 DB 1936 GAAGGACATTTCTACAAATATCCCTGGGATTTTATGAGATTTCTCTCAAAACTGTAAAAA 1995
 |||
 QY 1802 TCATGAAAAATAGGAATCTGTGAGAAACATCACAGACACATGAGACTAAGGAGACAT 1861
 |||
 DB 1996 TCATGAAAAATAGGAATCTGTGAGAAACATCACAGACACATGAGACTAAGGAGACAT 2055
 |||
 QY 1862 GTGAGCAAAATGCAATGTCTCTTTGGATCAGATCTCTGAGACAGAAAAAGATCAGTAATG 1921
 |||
 DB 2056 GTGAGCAAAATGCAATGTCTCTTTGGATCAGATCTCTGAGACAGAAAAAGATCAGTAATG 2115
 |||
 QY 1922 AAAAAACATGATGAGCTGAATATAGAAATCTGGAATATTTTAAAGAGTGTGATTTCTT 1981
 |||
 DB 2116 AAAAAACATGATGAGCTGAATATAGAAATCTGGAATATTTTAAAGAGTGTGATTTCTT 2175
 |||
 QY 1982 AATCTTGACAAATATATGACAGGTAATGTAAAGATGATACGTTAGAGAACTGAAACTGGG 2041

DB 2176 AATCTTGACAAATATATGACAGGTAATGTAAAGATGATACGTTAGAGAACTGAAACTGGG 2235
 |||
 QY 2042 TGAGGGCTATCTAGGAATTTCTGTACTATCTTACCAATTTTGGTAAAGTCTAAGAAAG 2101
 |||
 DB 2236 TGAGGGCTATCTAGGAATTTCTGTACTATCTTACCAATTTTGGTAAAGTCTAAGAAAG 2295
 |||
 QY 2102 CAATGCAA 2109
 |||
 DB 2296 CAACACTA 2303
 |||
 RESULT 7
 ABV25272
 ID ABV25272 standard; cDNA; 2452 BP.
 XX
 AC ABV25272;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25263.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PE 20-FEB-2001; 2001WO-US05171.
 XX
 PF 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1: Page 4961; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;
 XX
 Query Match. 97.9%; Score 2100; DB 23; Length 2452;
 Best Local Similarity. 99.8%; Pred. No. 0;
 Matches 2103; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY	2	GAGAAACAAATACCTTCATCCCTGCTCGAAGAACATCGAATGACATTTATCCCACTGCT	61
Db	196	GATGAAACAAATACCTTCATCCCTGCTCGAAGAACATCGAATGACATTTATCCCACTGCT	255
OY	62	GTTGTTCTGTGTTGGTGGGCTGCTTCATCTTTTCCAGCAAAATGAAGATTAAGATCCCGC	121
Db	256	GTTGTTCTGTGTTGGTGGGCTGCTTCATCTTTTCCAGCAAAATGAAGATTAAGATCCCGC	315
OY	122	TTTACTCGTTTGTATACCAACCCAAACAAGTGCAAAAGGGAGATGTGAATGAAGCAAA	181
Db	316	TTTACTCGTTTGTATACCAACCCAAACAAGTGCAAAAGGGAGATGTGAATGAAGCAAA	375
OY	182	TGAACGTGAGAGAGCAAGTATCTCCCCCTCCAGAAACATGCTGMAAGATGGAAATGAA	241
Db	376	TGAACGTGAGAGAGCAAGTATCTCCCCCTCCAGAAACATGCTGMAAGATGGAAATGAA	435
OY	242	AGAGCGTCGAGCAAAATGCCCAAAAGTGGGCAAAACAGTCGATTAACAGACAGTAACC	301
Db	436	AGAGCGTCGAGCAAAATGCCCAAAAGTGGGCAAAACAGTCGATTAACAGACAGTAACC	495
OY	302	AAAGATCGAAATGACAAAGTCTAAATAGTGGTGAATCTCTACATGTCAAGTCCCCAG	361
Db	496	AAAGATCGAAATGACAAAGTCTAAATAGTGGTGAATCTCTACATGTCAAGTCCCTCCAG	555
OY	362	CTCATGTGTACAAAGCAATCCAAAGCTGTGTTGATGAGTACATGATTTTGACTTTGGTGT	421
Db	556	CTCATGTGTGTACAAAGCAATCCAAAGCTGTGTTGATGAGTACATGATTTTGACTTTGGTGT	615
OY	422	AGGGCCAAAGACTCCCAACAGCAGATGTTGGACATTTATACAGAGTGTGTTGGTACTTTC	481
Db	616	AGGGCCAAAGACTCCCAACAGCAGATGTTGGACATTTATACAGAGTGTGTTGGTACTTTC	675
OY	482	ATACCTCGTTGATGTGGAATGCTTACTGTCTCCCAATCAAAAAGTTCTAAATATCTACTA	541
Db	676	ATACCTCGTTGATGTGGAATGCTTACTGTCTCCCAATCAAAAAGTTCTAAATATCTACTA	735
OY	542	TGTTGCCCAATATGTGCTCGCTGCTGTAATGGGCTAATAGCTATATGTCCCTTATGACA	601
Db	736	TGTTGCCCAATATGTGCTCGCTGCTGTAATGGGCTAATAGCTATATGTCCCTTATGACA	795
OY	602	AGAGCACCTTGTGCCAGTGTCCACAGATACCTGTGACGATGAGCTATGACCAACATGGTG	661
Db	796	AGAGCACCTTGTGCCAGTGTCCACAGATACCTGTGACGATGAGCTATGACCAACATGGTG	855
OY	662	CAAGTACGAAGATCTCTATATGTAAGTGTAAAGTTGAGCTACATTAACCTGTAAACA	721
Db	856	CAAGTACGAAGATCTCTATATGTAAGTGTAAAGTTGAGCTACATTAACCTGTGTAAACA	915
OY	722	TCAGTTGGTCAGGGAGAGTGTGAAGCATCTGCAATTTGTTCAACAGCAATTTTAAAT	781
Db	916	TCAGTTGGTCAGGGAGAGTGTGAAGCATCTGCAATTTGTTCAACAGCAATTTTAAAT	975
OY	782	ACGCATTACACACCGAGTAGGGCTATGTAGAGAGAGTCAAGATTATCTACTTAGATTGG	841
Db	976	ACGCATTACACACCGAGTAGGGCTATGTAGAGAGAGTCAAGATTATCTACTTAGATTGG	1035
OY	842	CATCTACTTAGATTTAACATATCTAGCTAGCTAGCAAAATGTAGGCATGTTGTATACATTT	901
Db	1036	CATCTACTTAGATTTAACATATCTAGCTAGCTAGCAAAATGTAGGCATGTTGTATACATTT	1095
OY	902	GATTCAAAATGTTTCTCTGTGATCGCTTTTATTTACAAAAATTTTTCATACAA	961
Db	1096	GATTCAAAATGTTTCTCTGTGATCGCTTTTATTTACAAAAATTTTTCATACAA	1155
OY	962	ATGGTAAAAAGAACAAATCTATACAACAACTTTGATTTTATATATAACTTTGT	1021
Db	1156	ATGGTAAAAAGAACAAATCTATACAACAACTTTGATTTTATATATAACTTTGT	1215
OY	1022	GATTAAATTTACTGAATTTAATTAAGGTGTAATTTTGAAGCTGTATCTCATATGAC	1081
Db	1216	GATTAAATTTACTGAATTTAATTAAGGTGTAATTTTGAAGCTGTATCTCATATGAC	1275

QY	1082	TAGTTCCTAAACACCCGGAGTTGAAAGTGAATTAATGTCCTAGAACAAATGTGCAA	1141
Db	1276	TAAGTTCCTAAACCCCTGGATGTAAGTGAATTAATGTCCTAGAACAAATGTGCAA	1335
QY	1142	AAGAACAATATAATTTTACATGAACCCCTTGGCTGTAGTTGCTTCTAGTCCACATC	1201
Db	1336	AAAGAACAATATAATTTTACATGAACCCCTTGGCTGTAGTTGCTTCTAGTCCACATC	1395
QY	1202	TAAAGCTAAGCATCTTCAAAGACGTTTTCCCATATGCTGCTTAATTCCTTCACTAAT	1261
Db	1396	TAAAGCTAAGCATCTTCAAAGACGTTTTCCCATATGCTGCTTAATTCCTTCACTAAT	1455
QY	1262	CACCCCTTCTCCCATCATCTGCGGCTGGCATCCTCCACATTAAGTTGAAGCTGTCCTCT	1321
Db	1456	CACCCCTTCTCCCATCATCTGCGGCTGGCATCCTCCACATTAAGTTGAAGCTGTCCTCT	1515
QY	1322	AAACATCTCGACTTTTATTTTGGCCAAATCAATACATCTTTGAATTTTATATCGC	1381
Db	1516	AAACATCTCGACTTTTATTTTGGCCAAATCAATACATCTTTGAATTTTATATCGC	1575
QY	1382	ATAAATTTTACAGTAGAATATGATCAAACTTCATTTTAAACCCCTTCTCTTTGACA	1441
Db	1576	ATAAATTTTACAGTAGAATATGATCAAACTTCATTTTAAACCCCTTCTCTTTGACA	1635
QY	1442	AAACTTCCTTAAAAAAGAAATACAGAATATATAGTAAATACCTCCACTCAAGAGGTA	1501
Db	1636	AAACTTCCTTAAAAAAGAAATACAGAATATATAGTAAATACCTCCACTCAAGAGGTA	1695
QY	1502	GAACCTAGTCCCTCCCTGGTAGTGGCTTCACTAAATAGAGACACCTCCCAAGAGATG	1561
Db	1696	GAACCTAGTCCCTCCCTGGTAGTGGCTTCACTAAATAGAGACACCTCCCAAGAGATG	1755
QY	1562	GAGTATGAAAGGAAACATAGTAACCTTTACAGGGGAGAAAAATGACAAATGACGCTTC	1621
Db	1756	GAGTATGAAAGGAAACATAGTAACCTTTACAGGGGAGAAAAATGACAAATGACGCTTC	1815
QY	1622	ACCAAGTAGTCAAAATTTAAGCTCACAGATGAATCAATTCGATTTGTCTAGATATTC	1681
Db	1816	ACCAAGTAGTCAAAATTTAAGCTCACAGATGAATCAATTCGATTTGTCTAGATATTC	1875
QY	1682	TTTTCTAAATTCATTAATCCCAATCTAATTAATGAGCTAAACATCCAGCAATCAAGTT	1741
Db	1876	TTTTCTAAATTCATTAATCCCAATCTAATTAATGAGCTAAACATCCAGCAATCAAGTT	1935
QY	1742	GAAGACATCTTCAAAATATATCCCTGGGCTATTTTAGAGTATTCCTCAAACTGTAAAA	1801
Db	1936	GAAGACATCTTCAAAATATATCCCTGGGCTATTTTAGAGTATTCCTCAAACTGTAAAA	1995
QY	1802	TCATGAAATATAGGGAATCTGAGAAACAAATCACAGACACATGACATAGATAGAGACAT	1861
Db	1996	TCATGAAATATAGGGAATCTGAGAAACAAATCACAGACACATGACATAGAGAGACAT	2055
QY	1862	GTGAGCCAATGCAATGTGCTTCTTGAGATCAGATCCTGTGAGACAGAAAAAGATCAATAATG	1921
Db	2056	GTGAGCCAATGCAATGTGCTTCTTGAGATCAGATCCTGTGAGACAGAAAAAGATCAATAATG	2115
QY	1922	AAAAAACTGATGAAGTCTGAATATAGATCTGAGAGTATTTTAAACAGTAGTGTGATTTCTT	1981
Db	2116	AAAAAACTGATGAAGTCTGAATATAGATCTGAGAGTATTTTAAACAGTAGTGTGATTTCTT	2175
QY	1982	AATCTTGACAAATATAGCAGGGATATGTATAGATGATACGTTAGAGAAACTGAACCTGGG	2041
Db	2176	AATCTTGACAAATATAGCAGGGATATGTATAGATGATACGTTAGAGAAACTGAACCTGGG	2235
QY	2042	TGAGGGCTATCTAGGAATTCCTGTACTATCTTACCAAAATTTTCGGTAAGTAAAGAAAG	2101
Db	2236	TGAGGGCTATCTAGGAATTCCTGTACTATCTTACCAAAATTTTCGGTAAGTAAAGAAAG	2295
QY	2102	CAATGCAA 2109	
Db	2296	CAACACTA 2303	

RESULT 8

ABV25706
ID ABV25706 standard; cDNA; 2452 BP.

AC ABV25706;

DT 16-SEP-2002 (flrst entry)

Human prostate expression marker CDNA 25697.

KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacokinetic marker

yy
yy
yy
Homo sapiens.

PN WO200160860-A2

PD 23-AUG-2001.

PF 20-FEB-2001;
yy

PR 17-FEB-2000; 2000US-183319P;
PR 16-MAR-2000; 2000US-199863P

PR 23-MAY-2000; 2000US-20/454P;
PR 09-JUN-2000; 2000US-211314P

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIV

PI. Schlegel R, Endege WO, Mon

DR WPI; 2001-662795/76.
YY

PT Novel isolated nucleic acid
prostate cells and correlati

XX
1:1
for detecting presence of prostate cancer,

XX

CC a nucleotide sequence

(a) assessing whether a patient is afflicted with prostate cancer;

cc (c) assessing the efficacy of a test compo
cc cancer in a patient:

CC (a), assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound

(h) assessing the aggressiveness or indolence of prostate cancer

(1) is also useful as a pharmacodynamic or pharmacogenomic marker

SV sequence 2452 BP; 181 A; 467 C; 444 G; 754 T; 0 other;

Best Local Similarity	99.88%;	Pred. No. 0;	DB 23;	Length 2452;
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REPORT OF THE
STANDARD, C. SERVICE UNIT

[illegible]

62

256 GTTGTTCCTGGTTGCTGGGCTGTTCCATCTTTTCCACCCAAATCAGACATACACATCCACCC

QY 122 TTTTACTGCTTTGTTAACCAACCAACACAAAGTGCMAAGGAGATTGTG

Db 316 TTTTACTGCTTGTTAACCAACCAACACACAGTGC AAGGAGATTGTGAATAAGCACAA 375

QY	182	TCACGTGAGGAGACAGTATCTCCCCCTGCGCAGAAACATGCTGTAAGTATGGAAACAA	241
Dp	376	TCACGTGAGGAGACAGTATCTCCCCCTGCGCAGAAACATGCTGTAAGTATGGAAACAA	435
QY	242	AGAGCGTCGACCAATGCCCCAAAAGTGGGCAAAACACAGTCGCAATTTACAGACAGTAACCC	301
Dp	436	AGAGCGTCGACCAATGCCCCAAAAGTGGGCAAAACACAGTCGCAATTTACAGACAGTAACCC	495
QY	302	AAAGAGTGGAAATGCAACTCTAAAATGCGGAGCAATCTCATATGTCAGTCCCCCAG	361
Dp	496	AAAGAGTGGAAATGCAACTCTAAAATGCGGAGCAATCTCATATGTCAGTCCCCCAG	555
QY	362	CTCATGGTCACAAAGCAATCCAAAGCTGGTTGATGAGTACATAGATTTGACTTTGGTGT	421
Dp	556	CTCATGGTCACAAAGCAATCCAAAGCTGGTTGATGAGTACATAGATTTGACTTTGGTGT	615
QY	422	AGGGCCAAAGACTCCCAACGCAAGTGGTGGACATTTACACAGGTGTTGGTACTCTTC	481
Dp	616	AGGGCCAAAGACTCCCAACGCAAGTGGTGGACATTTACACAGGTGTTGGTACTCTTC	675
QY	482	ATACCTCGTGGATGTGAAATGCCCTACTGCCCCCAATCAAAAAGTCTTAAATACTACTA	541
Dp	676	ATACCTCGTGGATGTGAAATGCCCTACTGCCCCCAATCAAAAAGTCTTAAATACTACTA	735
QY	542	TGTTTGCCCAATATTTGCTCTGCTGTAAATTTGGGCTAATAGACTATATGTCCCTATGACA	601
Dp	736	TGTTTGCCCAATATTTGCTCTGCTGTAAATTTGGGCTAATAGACTATATGTCCCTATGACA	795
QY	602	AGGACACACCTTGTCGACAGTTGCCAGATTCGACATCTGACAGTACTATGCAACCAATGGTTG	661
Dp	796	AGGACACACCTTGTCGACAGTTGCCAGATTCGACAGTACTATGCAACCAATGGTTG	855
QY	662	CAAGTACGAAAGATCTCTATAGTAAGTGTAAAAGTTTGAAGCTACATTAACCTGTAAACA	721
Dp	856	CAAGTACGAAAGATCTCTATAGTAAGTGTAAAAGTTTGAAGCTACATTAACCTGTAAACA	915
QY	722	TCAGTGTGTCAGGACAGTGGCAAGGCAATCCTCGCAATGTTTCAACAGCATTTATTAAT	781
Dp	916	TCAGTGTGTCAGGACAGTGGCAAGGCAATCCTCGCAATGTTTCAACAGCATTTATTAAT	975
QY	782	ACGCATTACACACCGAGTAGGGCTATGTAGAGAGAGTACGATTATCTACTTAGATTTGG	841
Dp	976	ACGCATTACACACCGAGTAGGGCTATGTAGAGAGAGTACGATTATCTACTTAGATTTGG	1033
QY	842	CATCTACTAGATTTAACTATACTAGCTAGAGAAATTTAGCGATGTTGATACACATTT	901
Dp	1036	CATCTACTAGATTTAACTATACTAGCTAGAGAAATTTAGCGATGTTGATACACATTT	1099
QY	902	GATTTCAAATGTTTTTCTCTGATCGCTTTTATTTATACAAAATATTTTTCATACAA	961
Dp	1096	GATTTCAAATGTTTTTCTCTGATCGCTTTTATTTATACAAAATATTTTTCATACAA	1155
QY	962	ATGCTTAAAAAGAAACAAATCTATACAAACAACCTTGGATTTTTTATATATAAAGTTGT	1021
Dp	1156	ATGCTTAAAAAGAAACAAATCTATACAAACAACCTTGGATTTTTTATATATAAAGTTGT	1215
QY	1022	GATTTAATTTACGATTTAATTTAGGGTAAATTTTCAAAAGTGTATATCTCATATGAC	1081
Dp	1216	GATTTAATTTACGATTTAATTTAGGGTAAATTTTCAAAAGTGTATATCTCATATGAC	1277
QY	1082	TAACTTCACTAAAACCTGTGATGAAGTGAATAATATGTCTCTAGAACAAATATGTACA	1144
Dp	1276	TAACTTCACTAAAACCTGTGATGAAGTGAATAATATGTCTCTAGAACAAATATGTACA	1333
QY	1142	AAAGAAACAATATATTTTTCATATGAACCTGTGGCTATGTTGCTTTCTAGCTCCACTC	1201
Dp	1336	AAAGAAACAATATATTTTTCATATGAACCTGTGGCTATGTTGCTTTCTAGCTCCACTC	1395
QY	1202	TAAAGCTTACACTTTCACAAAGAGTGTTCCTCCATATCTGTCTTAATCTTTTCACTACT	1261
Dp	1396	TAAAGCTTACACTTTCACAAAGAGTGTTCCTCCATATCTGTCTTAATCTTTTCACTACT	1455

OY	362	CTCATGGCACAAGCATCCAAAGCGGTGTGATGAGTCATAGATTTTGACTTTGGGT	421
Db	556	CTCATGGTCACAAAGCATCCAAAGCGGTGTGATGAGTCATAGATTTTGACTTTGGGT	615
OY	422	AGGCGCAAAAGCTCCCAAGCAGTGGTGGACATTTATACAGAGTGTGGTACTCTTC	481
Db	616	AGGGCCAAAAGCTCCCAAGCAGTGGTGGACATTTATACAGAGTGTGGTACTCTTC	675
OY	482	ATACCTCGTTGGATGTGGAAATGCTTACTGTGCCAATCAAAAAGTTCTTAAATACTACTA	541
Db	676	ATACCTCGTTGGATGTGGAAATGCTTACTGTGCCAATCAAAAAGTTCTTAAATACTACTA	735
OY	542	TGTTTGGCAATATTTGCTCGTCTGGTAAATGGGCTATATACATATATGCCCCCTATGAACA	601
Db	736	TGTTTGGCAATATTTGCTCGTCTGGTAAATGGGCTATATATGCCCCCTATGAACA	795
OY	602	AGGAGCACCTTGTGCGAGTTGCCAGATACTGTGAGATGGACATGCAACCAATGTTG	661
Db	796	AGGAGCACCTTGTGCGAGTTGCCAGATACTGTGAGATGGACATGCAACCAATGTTG	855
OY	662	CAATATAGAGAGATCTCATATGTAACGTGTAAATTTGAAGCTCCACATTTAACCTGTAAACA	721
Db	856	CAATATAGAGAGATCTCATATGTAACGTGTAAATTTGAAGCTCCACATTTAACCTGTAAACA	915
OY	722	TCAGTTGGTCAGGACAGTTGCAAAAGCATCTGCATTTGTTCAAAACAGATTATTAAT	781
Db	916	TCAGTTGGTCAGGACAGTTGCAAAAGCATCTGCATTTGTTCAAAACAGATTATTAAT	975
OY	782	ACGCATTACACCCGAGTAGGGCTATGTAGAGAGAGTCAGATTATCTACTAGATTTGG	841
Db	976	ACGCATTACACCCGAGTAGGGCTATGTAGAGAGAGTCAGATTATCTACTAGATTTGG	1035
OY	842	CATCTACTAATATTATACATATCTACTGCGAGAAATTGATAGCATGTTGATACACATT	901
Db	1036	CATCTACTAATATTATACATATCTACTGCGAGAAATTGATAGCATGTTGATACACATT	1095
OY	902	GATTTCAAAATGTTTTCTCTCGATCTGCTTTTATTTTACAAAATAATTTTTCATACAA	961
Db	1096	GATTTCAAAATGTTTTCTCTCGATCTGCTTTTATTTTACAAAATAATTTTTCATACAA	1155
OY	962	ATGCTTAAAAAAGAACAAATCTATACACAAACCTTGGATTTTATATATAAATTGTT	1021
Db	1156	ATGCTTAAAAAAGAACAAATCTATACAAACCTTGGATTTTATATATAAATTGTT	1215
OY	1022	GATTTAAATTTACTGATTTATATAGGGGTGAATAATTTGAAGTGTATTCATCATATAC	1081
Db	1216	GATTTAAATTTACTGATTTATATAGGGGTGAATAATTTGAAGTGTATTCATCATATAC	1275
OY	1082	TAAGTTCACTAAAAACCTGTGATGAAAGTGAATAATTTGTTCTGTAGAACAAAATGTACA	1141
Db	1276	TAAGTTCACTAAAAACCTGTGATGAAAGTGAATAATTTGTTCTGTAGAACAAAATGTACA	1335
OY	1142	AAAGAACATATATTTTACATGTAACCCCTGGCTGTAGTGGCTTCTCTAGCTCACTC	1201
Db	1336	AAAGAACATATATATTTTACATGTAACCCCTGGCTGTAGTGGCTTCTCTAGCTCACTC	1395
OY	1202	TAAAGCTAAGCATCTTCAAGAGCTTTTCCCATATCTGTCTTAATCTTTTCACCTCAAT	1261
Db	1396	TAAAGCTAAGCATCTTCAAGAGCTTTTCCCATATCTGTCTTAATCTTTTCACCTCAAT	1455
OY	1262	CACCCCTTCTCCCATCATCTGCGTGGCATCTCACAATTTGAGTGAAGCTTCTCTCT	1321
Db	1456	CACCCCTTCTCCCATCATCTGCGTGGCATCTCACAATTTGAGTGAAGCTTCTCTCT	1515
OY	1322	AAAACATCTCGACTTTTATTTTGCCAAAATCAATCAATCTTGAATTTTTTATCTGC	1381
Db	1516	AAAACATCTCGACTTTTATTTTGCCAAAATCAATCAATCTTGAATTTTTTATCTGC	1579
OY	1382	ATAAATTTTACAGTAAATATGATCAAACTCTATTTTAAACCTCTCTCTCTTGACA	1441
Db	1576	ATAAATTTTACAGTAAATATGATCAAACTCTATTTTAAACCTCTCTCTCTTGACA	1639

QY	1442	AACTTCCTTAAAAAGAAATCAAGATAAATATAGTAAATACCTCCACCTCAAGAGSTA	1501
Dd	1636	AAACTTCCTTAAAAAGAAATCAAGATATATATAGTAAATACCTCCACTCAAGAGSTA	1655
QY	1502	GAACCTCACTCCCTCCCTTGTGAGTCTTCACTAAATCACTAGTCACTTCCAAAGAGTG	1561
Dd	1696	GAACCTCACTCCCTCCCTTGTGAGTCTTCACTAAATCACTAGTCACTTCCAAAGAGTG	1755
QY	1562	GAGTGTGAAAAGGGAACATAGTAACTTTAAGGGGAGAAAAATGACAAATGACGTCTTC	1621
Dd	1756	GAGTGTGAAAAGGGAACATAGTAACTTTAAGGGGAGAAAAATGACAAATGACGTCTTC	1815
QY	1622	ACCAAGTATCAAAATTTAAGCTCAACCACTGATTAAGTCACTTGCATTTTCTTACATATATC	1681
Dd	1816	ACCAAGTATCAAAATTTAAGCTCAACCACTGATTAAGTCACTTGCATTTTCTTACATATATC	1875
QY	1662	TTTCTTAAAAATTCATATATCCCAATCTATTTATGAGCTTAAAAATCCAGCAAACTCAAGTT	1741
Dd	1876	TTTCTTAAAAATTCATATATCCCAATCTATTTATGAGCTTAAAAATCCAGCAAACTCAAGTT	1935
QY	1742	GAGGACATTCCTACAAATATCCCTGGGGTATTTTAGAGTATTCCTCCATAAAGCTATAAAA	1801
Dd	1936	GAGGACATTCCTACAAATATCCCTGGGGTATTTTAGAGTATTCCTCCATAAAGCTATAAAA	1995
QY	1802	TCATGAAAATTAAGGGAATCCTGAGAAAATCACAGACCACTAGACCTAAGAGACAT	1861
Dd	1996	TCATGAAAATTAAGGGAATCCTGAGAAAATCACAGACCACTAGACCTAAGAGAGACAT	2055
QY	1862	GTGACCCAAATGCAATGTGCTTCTTGATGCATGATCCTGAGACAAAAAAGATCAGTAAATG	1921
Dd	2056	GTGACCCAAATGCAATGTGCTTCTTGATGCATGATCCTGAGACAAAAAAGATCAGTAAATG	2115
QY	1922	AAAAAATGATGCACTGCAATAGATAGATGTGGAGTATTTTAAACAGTATGTGTTGATTTCTT	1981
Dd	2116	AAAAAATGATGCACTGCAATAGATAGATGTGGAGTATTTTAAACAGTATGTGTTGATTTCTT	2175
QY	1982	AATCTTGACAAATATAGCAGGGTATGTAAATGATGATTAACCTTAAGAGAACTGAAACTGGG	2041
Dd	2176	AATCTTGACAAATATAGCAGGGTATGTAAATGATGATTAACCTTAAGAGAACTGAAACTGGG	2235
QY	2042	TGAGGGCTATCTAGGAATTCCTGTACTACTCTTACCAATTTTGGTAAAGCTTAAGAAG	2101
Dd	2236	TGAGGGCTATCTAGGAATTCCTGTACTACTCTTACCAATTTTGGTAAAGCTTAAGAAG	2295
QY	2102	CAATGCAA	2109
Dd	2236	CAACACTA	2303
RESULT 10			
ABV28648			
ID	ABV28648	standard; cDNA; 2452 BP.	
XX	AC	ABV28648;	
XX	AC		
XX	DT	16-SEP-2002 (first entry)	
XX	DE	Human prostate expression marker cDNA 28639.	
XX	KW	Human; prostate cancer; cytosolic; carcinogen; pharmacodynamic marker	
XX	KM	pharmacogenomic marker; gene; ss.	
OS	XX	Homo sapiens.	
XX	PN	WO200160860-A2.	
XX	PD	23-AUG-2001.	
PF	20-FEB-2001;	2001WO-US05171.	
XX	17-FEB-2000;	2000US-183319P.	
PR	16-MAR-2000;	2000US-189862P.	
PR	25-MAY-2000;	2000US-207454P.	

PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX WPI: 2001-662795/76.
 DR
 PR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 6006; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 2452 BP: 787 A; 467 C; 444 G; 754 T; 0 other:
 Query Match 97.9%; Score 2100; DB 23; Length 2452;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2103; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 542 TGTGGCCAAATATGTCCTGCTGTAATTTGGGCTAATAGACTATATGTCCTTATGAAACA 601
 DB TGTGGCCAAATATGTCCTGCTGTAATTTGGGCTAATAGACTATATGTCCTTATGAAACA 795
 QY 602 AGGACACCTTGTGCGCACTTGGCCAGATACGTGTACATGACATGACATGACATGACATG 661
 DB AGGACACCTTGTGCGCACTTGGCCAGATACGTGTACATGACATGACATGACATGACATG 855
 QY 662 CAAGTACGAGATCTCTATAGTATGTAAGATGTAAGATGTAAGATGTAAGATGTAAGATG 721
 DB CAAGTACGAGATCTCTATAGTATGTAAGATGTAAGATGTAAGATGTAAGATGTAAGATG 915
 QY 722 TCAGTTGGTCAAGGACAGTGGCAAGCATCTGCAATGTTTCAACAGCATTTATTAAT 781
 DB TCAGTTGGTCAAGGACAGTGGCAAGCATCTGCAATGTTTCAACAGCATTTATTAAT 975
 QY 782 ACGCATTTACACACCGAGTAGGCTATGTAGAGAGAGATCAGATTTATCTACTAGATTGG 841
 DB ACGCATTTACACACCGAGTAGGCTATGTAGAGAGAGATCAGATTTATCTACTAGATTGG 1035
 QY 842 CATCTACTAGATTTAATACATATAGTACAGTAAGTATGAGCATGTTGATACATATT 901
 DB CATCTACTAGATTTAATACATATAGTACAGTAAGTATGAGCATGTTGATACATATT 1095
 QY 902 GATTTCAATATGTTTCTCTGATCTGCTTTTATTTACAAAATATTTTTCATACAA 961
 DB GATTTCAATATGTTTCTCTGATCTGCTTTTATTTACAAAATATTTTTCATACAA 1155
 QY 962 ATGTTTAAAGAAACAAATATATATACACAACTTTGATTTTATATATATATTTTGT 1021
 DB ATGTTTAAAGAAACAAATATATATACACAACTTTGATTTTATATATATATTTTGT 1215
 QY 1022 GATTTTAAATTTCTGATTTTAAATTTAGGTAAGTATTTGAAAGTATTTTCATATGAC 1081
 DB GATTTTAAATTTCTGATTTTAAATTTAGGTAAGTATTTGAAAGTATTTTCATATGAC 1275
 QY 1082 TAAGTACATTAACCTGATTTGAAAGTAAATATATTTCTTACAAACAAATATGACAA 1141
 DB TAAGTACATTAACCTGATTTGAAAGTAAATATATTTCTTACAAACAAATATGACAA 1335
 QY 1142 AAAGAAATATATATTTTACATGAACTTGGCTGTAGTGGCTTTCTTACATGACATC 1201
 DB AAAGAAATATATATTTTACATGAACTTGGCTGTAGTGGCTTTCTTACATGACATC 1395
 QY 1202 TAAGCTAGCATCTTCAAGAGCTTTCCCATGCTCTTCAATCTTCAATCTTCAATCT 1261
 DB TAAGCTAGCATCTTCAAGAGCTTTCCCATGCTCTTCAATCTTCAATCTTCAATCT 1455
 QY 1262 CACCTTCTTCCCAATCATCTGCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCT 1321
 DB CACCTTCTTCCCAATCATCTGCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCT 1515
 QY 1322 AAAACATCTCTGACTTTTATTTTGGCAAAATCAATCAATCTTGAATTTTATCTGC 1381
 DB AAAACATCTCTGACTTTTATTTTGGCAAAATCAATCAATCTTGAATTTTATCTGC 1575
 QY 1382 ATTAATTTTACAGTATATGATCAAACTTCAATTTTAACTCTCTCTCTCTGACA 1441
 DB ATTAATTTTACAGTATATGATCAAACTTCAATTTTAACTCTCTCTCTCTCTCTGACA 1635
 QY 1442 AAACCTCTTAAAGAAATACAAAGATATATAGTAAATACCTTCACTCAAGAGGTA 1501
 DB AAACCTCTTAAAGAAATACAAAGATATATAGTAAATACCTTCACTCAAGAGGTA 1695
 QY 1502 GAATCTAGTCT 1561
 DB GAATCTAGTCT 1755
 QY 1562 GAGTATGAAAGGAAATATAGTATTTTACAGGAGAAATATGACAAATGACATCTTC 1621
 DB GAGTATGAAAGGAAATATAGTATTTTACAGGAGAAATATGACAAATGACATCTTC 1815

OY 1622 ACCAAGTGAATCAAAATTAAGTCACAGTATAGTCAATTCAGATTGTTCTAGATATC 1681
 DB 1816 ACCAAGTGAATCAAAATTAAGTCACAGTATAGTCAATTCAGATTGTTCTAGATATC 1875
 OY 1682 TTTCTAAAATTCATATATCCCAATCTAATTATAGAGCTAAAACATCCAGCAAACTCAAGTT 1741
 DB 1876 TTTCTAAAATTCATATATCCCAATCTAATTATAGAGCTAAAACATCCAGCAAACTCAAGTT 1935
 OY 1742 GAAGGACATTCACAAATATATCCCGGATTTTATAGAGTATCCCAAACTGTAATAA 1801
 DB 1936 GAAGGACATTCACAAATATATCCCGGATTTTATAGAGTATCCCAAACTGTAATAA 1995
 OY 1802 TCATGAAAAATAGAGGAATCTCTGAGAAACATCACAGACCACATGAGACTTAAGAGACAT 1861
 DB 1996 TCATGAAAAATAGAGGAATCTCTGAGAAACATCACAGACCACATGAGACTTAAGAGACAT 2055
 OY 1862 GTGAGCCAAATGCAATGTCTTCTTGTGATCAGATCCTGAGACAGAAAAGATCAGTAATG 1921
 DB 2056 GTGAGCCAAATGCAATGTCTTCTTGTGATCAGATCCTGAGACAGAAAAGATCAGTAATG 2115
 OY 1922 AAAAACTGATGAGTCTGATAGAAATCTGAGATTTTAAACAGTATGATTTCTT 1981
 DB 2116 AAAAACTGATGAGTCTGATAGAAATCTGAGATTTTAAACAGTATGATTTCTT 2175
 OY 1982 AATCTTGACAAATATAGCAGGGTAATGTAAGATGATTAACGTTAGAGAACTGAACTGGG 2041
 DB 2176 AATCTTGACAAATATAGCAGGGTAATGTAAGATGATTAACGTTAGAGAACTGAACTGGG 2235
 OY 2042 TGAGGCTATCTAGGAATCTCTGTAATCTTACCAAAATTTTCGGTAAGTCTAAGAAAG 2101
 DB 2236 TGAGGCTATCTAGGAATCTCTGTAATCTTACCAAAATTTTCGGTAAGTCTAAGAAAG 2295
 OY 2102 CAATGCAA 2109
 DB 2296 CAACACTA 2303
 RESULT 11
 ABV24823
 ID ABV24823 standard; cDNA: 1610 BP.
 AC ABV24823;
 DT 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 24814.
 DE Human prostate expression marker cDNA 24814.
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PF 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 PT

PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 4758-4759; 11750pp; English.
 PS
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1610 BP; 543 A; 292 C; 292 G; 483 T; 0 other;
 Query Match 52.7%; Score 1130.6; DB 23; Length 1610;
 Best Local Similarity 99.6%; Pred. No. 3.4e-210;
 Matches 1133; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 2 GATGAACAAATACCTTCATCTGCTCTGGAACCACTGCATGACATTAATCCAGTGT 61
 DB 474 GATGAACAAATACCTTCATCTGCTCTGGAACCACTGCATGACATTAATCCAGTGT 533
 OY 62 GTTGTTCCTGCTGCTGGGCTGCTTCATCTTTCCAGCAATGAAGATAGATCCGC 121
 DB 534 GTTGTTCCTGCTGCTGGGCTGCTTCATCTTTCCAGCAATGAAGATAGATCCGC 593
 OY 122 TTTTACTGCTTTGTTAACCAACCAACACACTGCAAGGAGATTGCAATAAACACAA 181
 DB 594 TTTTACTGCTTTGTTAACCAACCAACACACTGCAAGGAGATTGCAATAAACACAA 653
 OY 182 TGAAGTGAAGAGAGAGATATCTCCCTCCGAAACATGCTGAAGATGAATGGAACAA 241
 DB 654 TGAAGTGAAGAGAGAGATATCTCCCTCCGAAACATGCTGAAGATGAATGGAACAA 713
 OY 242 AGAGGCTGACGCAATGCCCCCAAAAGTGGCAACAGTGAATTAACAGACAGTAAACC 301
 DB 714 AGAGGCTGACGCAATGCCCCCAAAAGTGGCAACAGTGAATTAACAGACAGTAAACC 773
 OY 302 AAAGGATCGAATGACAAGCTTAAATGTGTGAGAAATCTCTCAATGCTCAAGTCCCAAG 361
 DB 774 AAAGGATCGAATGACAAGCTTAAATGTGTGAGAAATCTCTCAATGCTCAAGTCCCAAG 833
 OY 362 CTGATGTCACAAAGCAATCCAAAGCTGTTGATGATGATCAATGATTTGACTTTGGTGT 421
 DB 834 CTGATGTCACAAAGCAATCCAAAGCTGTTGATGATGATCAATGATTTGACTTTGGTGT 893
 OY 422 AGGCGCAAGACTCCCAAGCAGAGTGTGACATTAACAGAGTGTGTTGGTACTTTC 481
 DB 894 AGGCGCAAGACTCCCAAGCAGAGTGTGACATTAACAGAGTGTGTTGGTACTTTC 953
 OY 482 ATACTGCTGATGATGGAATGCTACTGCTCCCAATGCAATGCAATGCAATGCAATGCA 541
 DB 1014 ATACTGCTGATGATGGAATGCTACTGCTCCCAATGCAATGCAATGCAATGCAATGCA 601
 OY 542 TGTGTCCAATATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 601
 DB 1014 TGTGTCCAATATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1073
 OY 602 AGGAGACCTTGTGCACTGCTCCAGATGATGATGATGATGATGATGATGATGATGATG 661
 DB 1074 AGGAGACCTTGTGCACTGCTCCAGATGATGATGATGATGATGATGATGATGATGATG 1133
 OY 662 CAAGTACGAGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 721
 DB 1134 CAAGTACGAGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1193

CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound;
CC	(g) determining whether prostate cancer has metastasized in a patient;
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX	
XX	Sequence 677 BP; 170 A; 143 C; 127 G; 233 T; 4 other;
SO	
SO	Query Match 26.6%; Score 569.4; DB 23; Length 677;
SO	Best Local Similarity 98.8%; Pred. No. 2.3e-101;
SO	Matches 592; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
OY	1470 ATATAGCTAAATACCTCCACCTCAAGAGAGTGAAGTACAGTCCCTCCCTGTGAGTCTT 1529
OY	
DB	677 ATATAGCTAAATTCCTCCACCTCAAGAGAGTGAAGTACAGTCCCTCCCTGTGAGTCTT 618
OY	1530 CACTAAATCACTGACTCACTCTCCAAAGAGTGGAGTATGGAAGGAAACATAGTAACTT 1589
OY	
DB	617 CACTAAATCACTGACTCACTCTCCAAAGAGTGGAGTATGGAAGGAAACATAGTAACTT 558
OY	1590 TACAGGGAGAAAATGACAAATGACGCTTATCCCAAGTATGCAAAATTAAGTACACCG 1649

OY	1650	TGATAAGTCATTCACATTGTCTCTAGATTAATCTTTCTAAAAATGCATATGCCAATCTAA	1709
Dd	497	TGATAGTCATTCACATTTGTTCTAGATTAATCTTCTAAAAATCTAAATCCCAATCTAA	438
OY	1710	TTATAGAGCTAAACAATCCAGCAAACCTCAAGTTGAAGGACATTCACAAAATATCCCTGGG	1769
Dd	437	TTATAGAGCTAAACAATCCAGCAAACCTCAAGTTGAAGGACATTCACAAAATATCCCTGGG	378
OY	1770	GTAATTTTAGAGTATTCCTCAAAACTGTAAAAATCATGGAATAATGCGGAATCCTAGAAA	1829
Dd	377	GTAATTTTAGAGTATTCCTCAAAACTGTAAAAATCATGGAATAATGCGGAATCCTAGAAA	318
OY	1830	CATACACAGACCACATGAGACTPAGGAGACATGTGAGCCAAATGCATGTGCTTCTTGA	1889
Dd	317	CATACACAGACCACATGAGACTPAGGAGACATGTGAGCCAAATGCATGTGCTTCTTGA	258
OY	1890	TCAGATCCTGGGAACAGAAAAACATCAGTAAATGAAAAAACTGATGAAGTGTGAATAGAATC	1949
Dd	257	TCAGATCCTGGGAACAGAAAAACATCAGTAAATGAAAAAACTGATGAAGTGTGAATAGAATC	198
OY	1950	TGAGATATTTTTAACAGTATGTGTGATTTCTTAATCTTGACAAATATATACAGGGTAATGT	2009
Dd	197	TGAGATATTTTTAACAGTATGTGTGATTTCTTAATCTTGACAAATATATACAGGGTAATGT	140
OY	2010	AAGATGATTAACGTTAGAGAAACTGAAACCTGGGTGAGGCTATCTTAGGAATTCCTGTAC	2068
Dd	139	AAGATGATTAACGTTAGAGAAACTGAAACCTGGGTGAGGCTATCTTAGGAATTCCTGTAC	81
RESULT 13			
ID	ABV08220/c		
XX	ABV08220 standard; CDNA; 676 BP.		
AC	ABV08220;		
XX			
DT	13-SEP-2002 (first entry)		
XX			
DE	Human prostate expression marker cDNA 8211.		
XX			
KX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;		
XX	pharmacogenomic marker; gene; ss.		
XX			

OS Homo sapiens.
 XX WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX WPI: 2001-662795/76.
 DR
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 1309; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 CC Sequence 676 BP; 181 A; 129 C; 123 G; 238 T; 5 other;
 XX
 SQ
 Query Match 26.2%; Score 561.4; DB 23; Length 676;
 Best Local Similarity 95.9%; Pred. No. 8.3e-100;
 Matches 627; Conservative 0; Mismatches 21; Indels 6; Gaps 5;

OY 1417 TTTTAACTCTCTCTCTTTGACAAAACCTCTTAAAAAGAAATACAAATATATAGG 1476
 DB 675 TTTTAACTCTCTCTCTTTGACAAAACCTCTTAAAAAGAAATACAAATATATAGG 616
 OY 1477 TAAATACCTCCACATCAAGAGAGTAGACTAGTCTCTCCCTTGAGTCTTCACTAAA 1536
 DB 615 TAAATCCCTCCACATCAAGAGAGTAGACTAGTCTCTCTCTTGAGTCTTCACTAAA 556
 OY 1537 ATCAGTACTACTCTCAAGAGAGTAGAGTAAAGGAAACATATAGTCTTACAGAG 1596
 DB 555 ATCAGTACTACTCTCAAGAGAGTAGAGTAAAGGAAACATATAGTCTTACAGAG 497
 OY 1597 GAGAAAAATGACAAATGAGCTTCA-CCAAGTGATCAAAATTAACGTCACACAGATAA 1655
 DB 496 GAGAAAAATGACAAATGAGCTTCA-CCAAGTGATCAAAATTAACGTCACACAGATAA 437
 OY 1656 GTCAATCAGATTGTGTAGATAATCTTTCTAAAAATTCATATCCCATC-TAATTATG 1714
 DB 436 GTCAATCAGATTGTGTAGATAATCTTTCTAAAAATTCATATCCCATC-TAATTATG 377
 OY 1715 AGCTAAAAATCCAGCAATCAAGTTGAAGACATTTACAAAATATCCCTGGGATAT 1774
 DB 376 AGCTAAAAATCCAGCAATCAAGTTGAAG-CAATCTACAAAATATCCCTGGGATAT 318

OY 1775 TTAGAGTATCTCTCAAACTGTAAAAATCATGAAAAATAGGAATCTGTAGAAAATC 1834
 DB 317 TTAGAGTATCTCTCAAACTGTAAAAATCATGAAAAATAGGAATCTGTAGAAAATC 258
 OY 1835 ACAGACACATGAGACTAGAGACATGTGACCAATGCAATGCTCTTGGATGCA 1894
 DB 257 ACAGACACATGAGACTAGAGACATGTGACCAATGCAATGCTCTTGGATGCA 198
 OY 1895 TCCTGGACAGAAAAAGATCACTAATGAAAAAACTGATGACTGATAGATCTGGAG 1954
 DB 197 TCCTGGACAGAAAAAGATCACTAATGAAAAAACTGATGACTGATAGATCTGGAG 138
 OY 1955 TATTTTAACTAGTGTGATTTCTTAATCTTGACAAATATAGCAGGTAATGTAGAT 2014
 DB 137 TATTTTAACTAGTGTGATTTCTTAATCTTGACAAATATAGCAGGTAATGTAGAT 80
 OY 2015 GATAAGCTTAGCAAACTGAACCTGGTGAGGCGTATCTAGAAATCTCTGTAC 2068
 DB 79 GATAAGCTTAGCAAACTGAACCTGGTGAGGCGTATCTAGAAATCTCTGTAC 26
 RESULT 14
 AAS70843.
 .ID AAS70843 standard; CDNA; 1386 BP.
 XX
 AC AAS70843;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #6647.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSEQ-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR P-PSDB; ABG06656.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID No 6647; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in

